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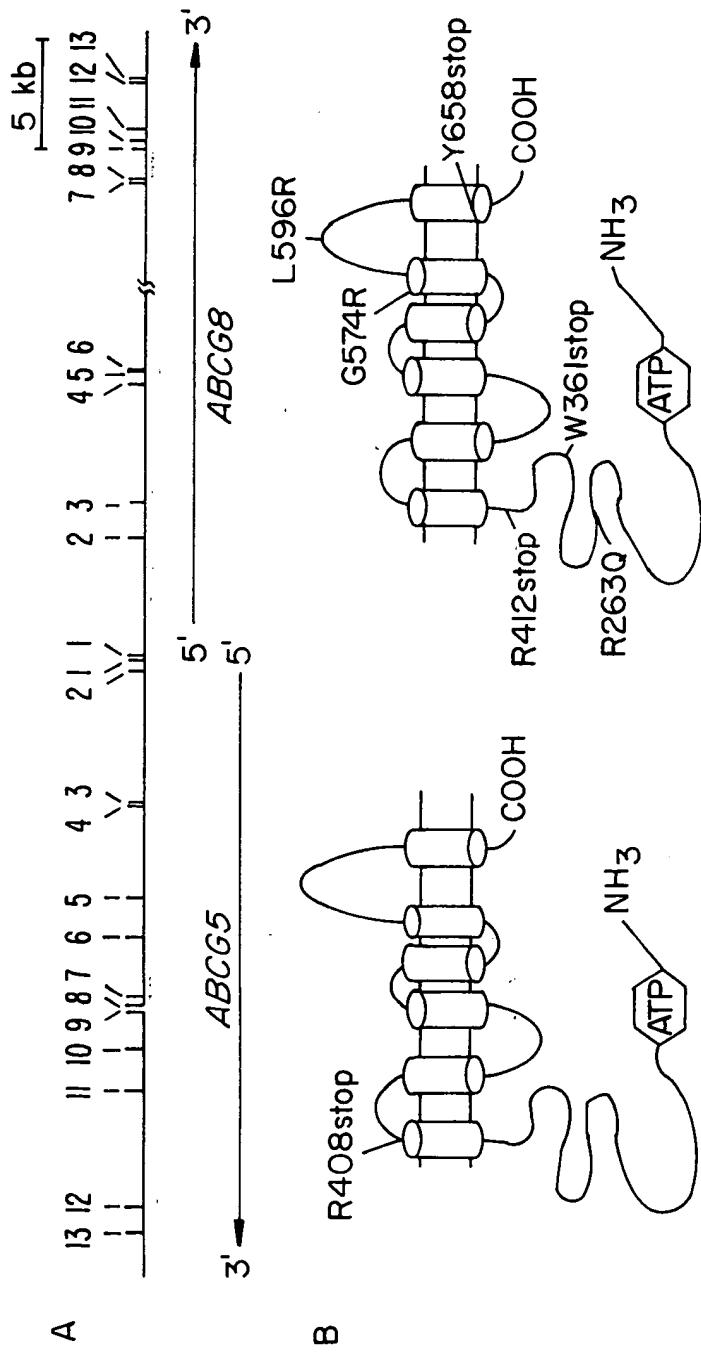


FIG. 1.



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ABCG5 M -----[GDISSLTPEGGSMGLQVNRCQSOSLEGAPAT-APEPHSI[GILHASYSU]SHRVR-[PW]-----  
 ABCG8 [MAGKAAEERGLPKGATPQDTSGLQDRLESSEDNSNLYFTYSGQENTLEVRDLYQVDLASQV[PW]FEQLAQ 54  
 70

ABCG5 ----[WDTISCRQOWTROIQLKDV[LY]ESGGIMC]LGSSGSGKTTILDAMS[GRLGRAGTFL-[GEVYV[N]GRA 119  
 ABCG8 FKMPWTPSC-[QNSCELGQNI[SFKY]RSQMLAI]IGSSGCGRASLLDVITGR-[GHGKIKSGQIWIN[GQP 136  
 208

ABCG5 LRREQFQDFSYM[Q]OSDTI[S]STVRET[I]HYTALLAIRF[G-NPGSFQ[KVEA]VMAETIS[SHVADRLIGNY 188  
 ABCG8 SSPQLVRRQVAHM[RQHNQI]LPNLTVRETIAFIAQMRLPRTFSQAQRD[KRVEDVIAEIRLIRQCADTRVGNM 208

ABCG5 SLGGIS[TGERRVS]AAQ[Q]IDPKVMLFDEPT[G]LDCMTANQI[V]VLDVE[TARRNR]IVVLT[HOPRSEI[FQ 258  
 ABCG8 YVRGL[S]GGERRVSIGV[Q]LIWNE[GILIL]DEPT[G]LDSFTAHNLVKTLSR[AKGNR]LYLIS[HOPRS]DIER 278

ABCG5 [LFDKIAILS[GELI]FCGT[PAEM]LDF[NDCGYPCPEHSN]FDFYM[DILTSVDTQSKERFIE[TSKRVQ]MIESA 328  
 ABCG8 [LEDLVLLMTSGTPIYI[GAAQH]VQYETAIGYPCPRYSN[PADFYV]DILTSIDRRSREQELA[REKAQ]SLLAAL 348

ABCG5 YDDSA-----ICHKT[LN]IERMKHLKT--L[P]M-----V[P]EKTRDSSP[G]VFSKLGV[IR]RVTRN[L]VRNKLAV 386  
 ABCG8 FLEKVRDLDDFLWKAET[K]DLD[DET]CVESSVT[BL]DTNC[LP]SPTK-[MPGAVQQFTT]L[RR]QIS[ND]FRLPTL 417

ABCG5 ITRLLQNLIM[GFLI]FV[IR]VRSNVLKGAIO[DRVGLI]YQFVFAT[P]YTGM[NAVNLFPVIRAVSDQE[SQDG 456  
 ABCG8 LIHGAECIMSMTIGE-[LYFGHGSIQLSFM]DTA[LL]FMI[GALI]EFNVI[DV]ISKCYSER[AM]LY[EL]DG 485

ABCG5 [LYQKWQMMIAYA]HVL[P]FSVVATM[F]ESSVCYWTLG[H]PEVAR[FGYFSAA]LLAPHLIGEFLT[V]LLGIVQN 526  
 ABCG8 LYTTGPFYF[EAKI]GELPEHCAYII[YGMPTYWLAN]R[RG]LQ[ELLHFLLVWLVVFC]CRIMAL[AA]ALLPT 555

**FIG. 1C.**



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ABCG5 PNIVNSVVALSIAGVVSGFLRNIQEM-PIPEKISYFTOKCSEIIVVNEFYGLNFTCGSSNVSVT 595  
ABCG8 FHMASFESNALYNSFYLAG-GEMINLSSLWTVE-AWISKVSELRWCEGLIMKIQESRRTYKMPLGNILTIA 623

ABCG5 TNPMCAFTQGIQFEKTCPGATSRFTMNFLYSFIPALVIGIVVFKIRDHLISR-- 651  
ABCG8 VS---GDKILSAMELDSYPLYAI-YLVIGLSGGMVIYVSLRFIKQKPSQD 673

Walker A Hotif  
Walker B Hotif  
Signature C-Hotif

**FIG. 1C. (CONTINUED)**



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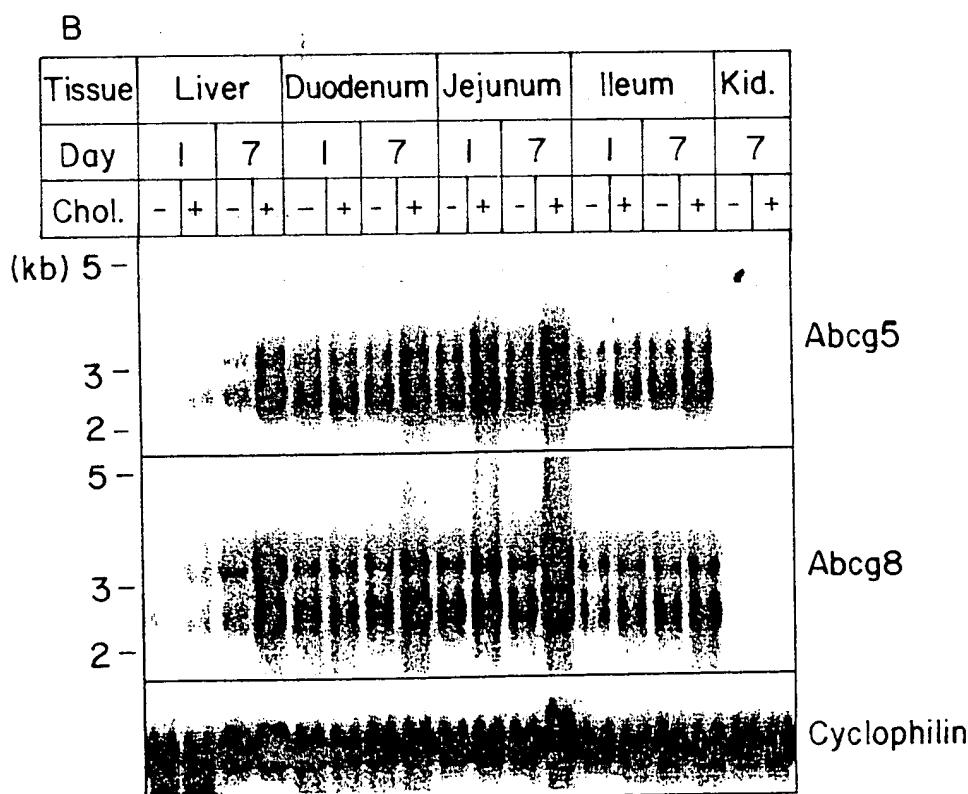
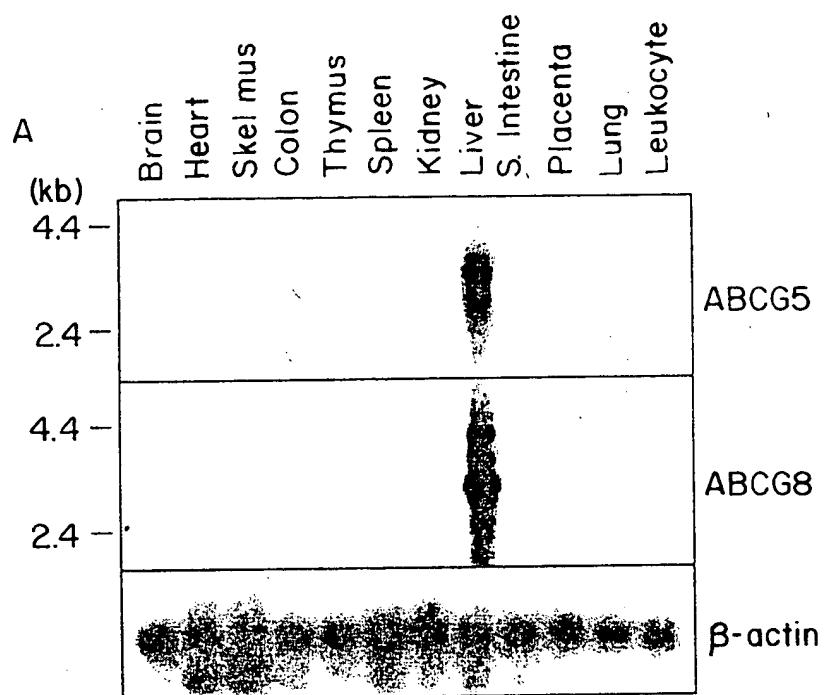


FIG. 2.



4 ABCG8 exon 2 (reverse strand) thru ABCG5 exon 2 (forward strand)

FIG. 3.

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gatttatatccactcaggaaaggcatcaaaggacgttattccatagacgtctgcctcatgggattctg  
caggaggttgcgttgcgttgcattctgttttgtccaggcaatccgttccccttccatggggactgggg  
ctgttgaatgtggccatccgttcttgttttgtccaggaaaatgggggggggggggggggggggggg  
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ggtaatgg  
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acaggggccctgcggcccccatttcatttgcggcagggttgcatttgcggcccccatt  
tctgacactgccttcggccatccatttgcggcagggttgcacttgcggcccccatt  
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ctggggcacttgcggcccccatttgcggcccccatttgcggcccccatttgcgg  
CTGGCTTATTGTGAGATAAGGACACTCTGGCTAAAGGTACATCAGATAATGG  
caggattccaggggctgggtaggatcggacaggggactccatggccatggccat  
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ACAGAGGGGTCTCTGAGCTCCCTGGAGCAAGGTCTGGTCA  
CAGCGTCAGgttaaggggacccacaggcaaaaaggtaggttgcatttgc  
gggttgtctgtccaggcaggatcagggtgaaaatggggacttgc  
gagcctggacataaaacatgcctggcttgcgttgc  
cacctgtccctgttagatgggggggggggggggggggggggg  
ggttcacttcaagaaggaaaggcaggatccatccagggtt  
ctccgtgggtggccaaacttgcatttgcggccat  
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**FIG. 3. (CONTINUED)**



The 4 exons are underlined and the conserved regions are in uppercase. The sequence ends in intron 2 of ABCG5 and is in the following order:

ABCG8 exon 2 (reverse strand)  
ABCG8 intron 1 (reverse strand)  
ABCG8 exon 1 (reverse strand)

**FIG. 3.** (CONTINUED)



### Gap between genes

ABCG5	exon 1	(forward strand)
ABCG5	intron 1	(forward strand)
ABCG5	exon 2	(forward strand)
ABCG5	intron 2	(forward strand, partial)

## B. Sequence Between ABCG5 and ABCG8 Containing the Control Sequences

FIG. 3. (CONTINUED)

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